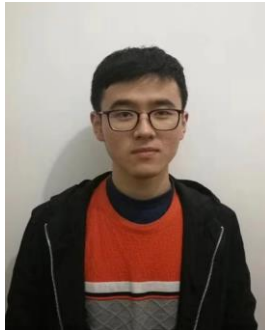




BRIGHT: A Bridging Algorithm for Network Alignment

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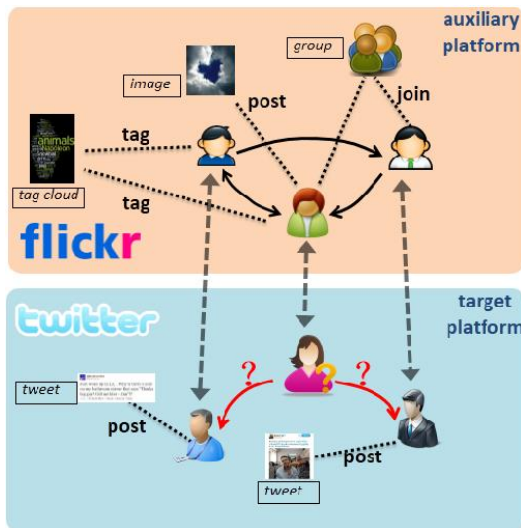
Outline

- Introduction
- Theoretical Analysis
- Proposed Model
- Experimental Results
- Conclusions

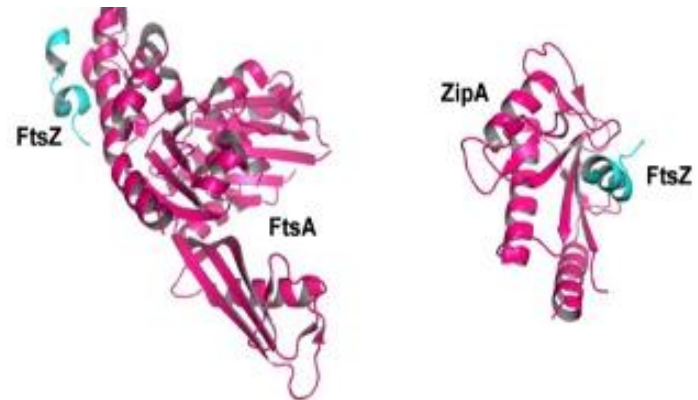
Network Alignment

- Networks are often multi-sourced
- To find node correspondence across networks

Friend recommendation

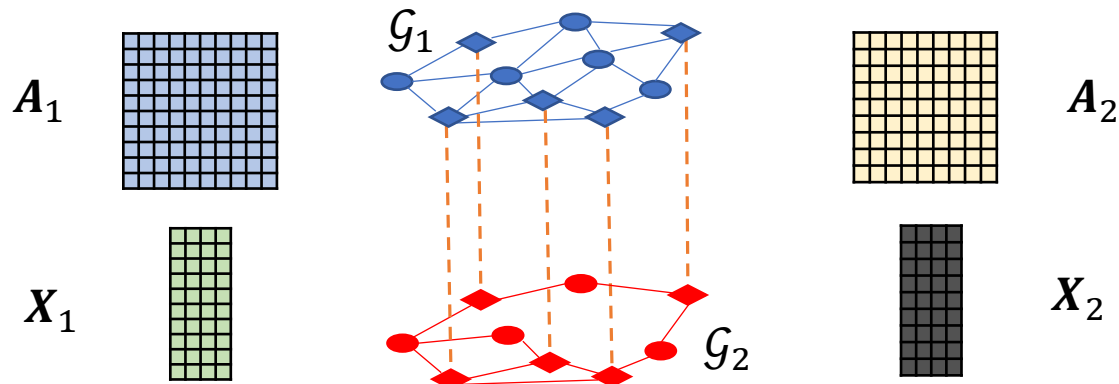


Drug design



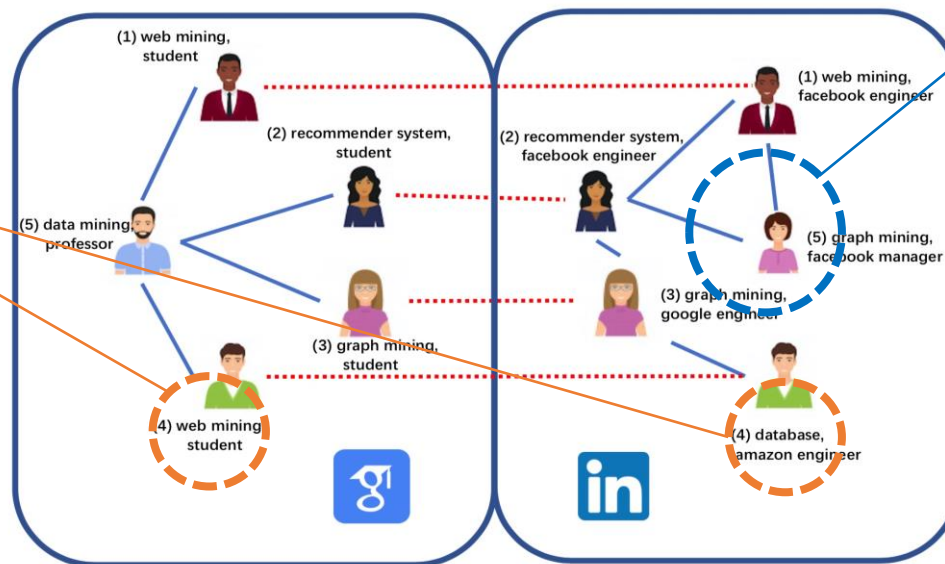
Prob. Def.: Semi-Supervised Attributed Network Alignment

- **Given:** (1) two attributed networks $\mathcal{G}_1 = \{A_1, X_1\}$, $\mathcal{G}_2 = \{A_2, X_2\}$; (2) a set of anchor node pairs L .
- **Output:** an $n_2 \times n_1$ alignment/similarity S .
- Scenario variants:
 - Semi-supervised plain network alignment (without X_1, X_2)
 - Unsupervised attributed network alignment (without L)



Existing Methods: Limitation #1

- Consistency optimization based methods
 - Consistency assumption violation:
 - (1) Attribute change
 - (2) Local topology change

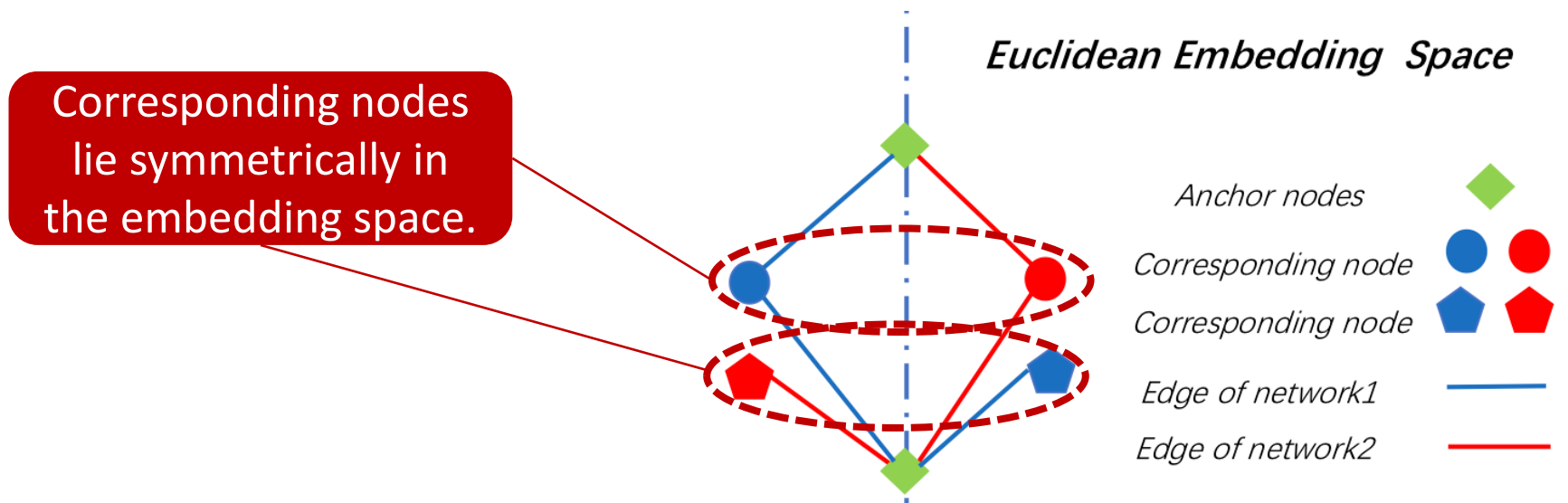


[1] Danai Koutra, Hanghang Tong, and David Lubensky. 2013. Big-align: Fast bipartite graph alignment. In 2013 IEEE 13th International Conference on Data Mining. IEEE, 389–398.

[2] Rohit Singh, Jinbo Xu, and Bonnie Berger. 2008. Global alignment of multiple protein interaction networks with application to functional orthology detection. Proceedings of the National Academy of Sciences 105, 35 (2008), 12763–12768.

Existing Methods: Limitation #2

- Embedding based methods
 - Introduce the space disparity issue



[1] Li Liu, William K Cheung, Xin Li, and Lejian Liao. [n.d.]. Aligning Users across Social Networks Using Network Embedding.

Outline

- Introduction ✓
- **Theoretical Analysis**
- Proposed Model
- Experimental Results
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Theoretical Analysis #1

Main Claim/Insight: Consistency optimization based methods are essentially random walk propagation of anchor links.

- Drawbacks

- Exactly same steps

- Equal weight for all anchor links

$$O_c(S) = \alpha \sum_{a,b,x,y} \left[\frac{S(x,a)}{\sqrt{d_2(x)d_1(a)}} - \frac{S(y,b)}{\sqrt{d_2(y)d_1(b)}} \right]^2 A_1(a,b) A_2(x,y) + (1-\alpha) \|S - H\|_F^2$$

1. Topology Consistency

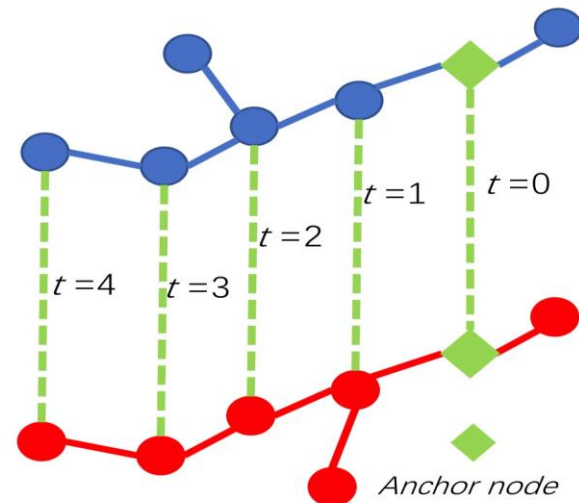
2. Known Anchor Links

$$s = (1 - \alpha)(I - \alpha \hat{W})^{-1} h$$

$$W = A_1 \otimes A_2$$

$$s(i) = (1 - \alpha) \sum_{j=0}^{n_2 \times n_1 - 1} \sum_{t=0}^{\infty} \alpha^t \hat{W}^t(i, j) \mathbb{1}(h(j))$$

Objective function solutions



[1] Rohit Singh, Jinbo Xu, and Bonnie Berger. 2008. Global alignment of multiple protein interaction networks with application to functional orthology detection. Proceedings of the National Academy of Sciences 105, 35 (2008), 12763–12768.

[2] Si Zhang and Hanghang Tong. 2016. Final: Fast attributed network alignment. In Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. 1345–1354.

Theoretical Analysis #2

Main Claim/Insight: Embedding based methods relax the objective function of consistency optimization based methods.

- Drawback
 - Space disparity

$$O_1^{in} = \sum_a (d(a, b) - d(a, c)) \quad O^{cross} = \sum_{(l_1, l_2) \in \mathcal{L}} d(l_1, l_2)$$

In a simple K -regular graph:

Two parts of loss

Consistency method loss

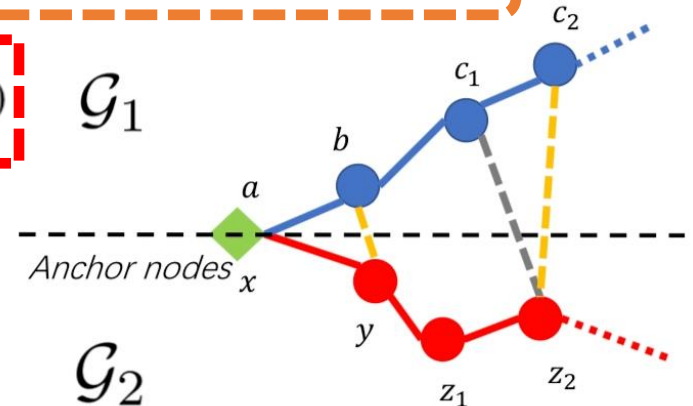
$$O_c(S) = \frac{1}{K^2} (1 - e^{-d(y, b)})^2 A_1(a, b) A_2(x, y)$$

Embedding method loss

$$O = d(b, a) + d(a, x) + d(x, y)$$

Relaxation relation

$$d(b, y) \leq d(b, a) + d(a, x) + d(x, y)$$



[1] Xiaokai Chu, Xinxin Fan, Di Yao, Zihua Zhu, Jianhui Huang, and Jingping Bi. 2019. Cross-Network Embedding for Multi-Network Alignment. In The World Wide Web Conference (WWW '19). ACM, New York, NY, USA, 273–284.

<https://doi.org/10.1145/3308558.3313499>

[2] Li Liu, William K Cheung, Xin Li, and Lejian Liao. [n.d.]. Aligning Users across Social Networks Using Network Embedding.

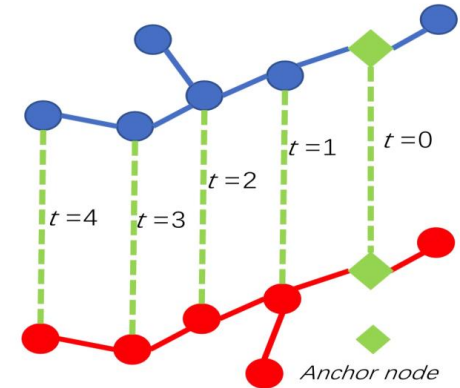
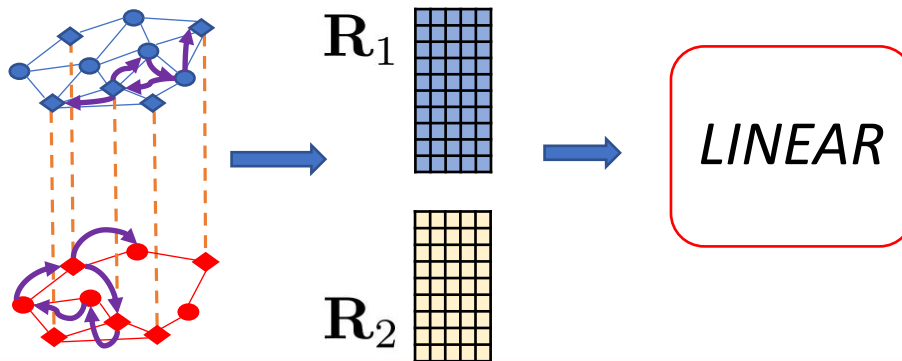


Outline

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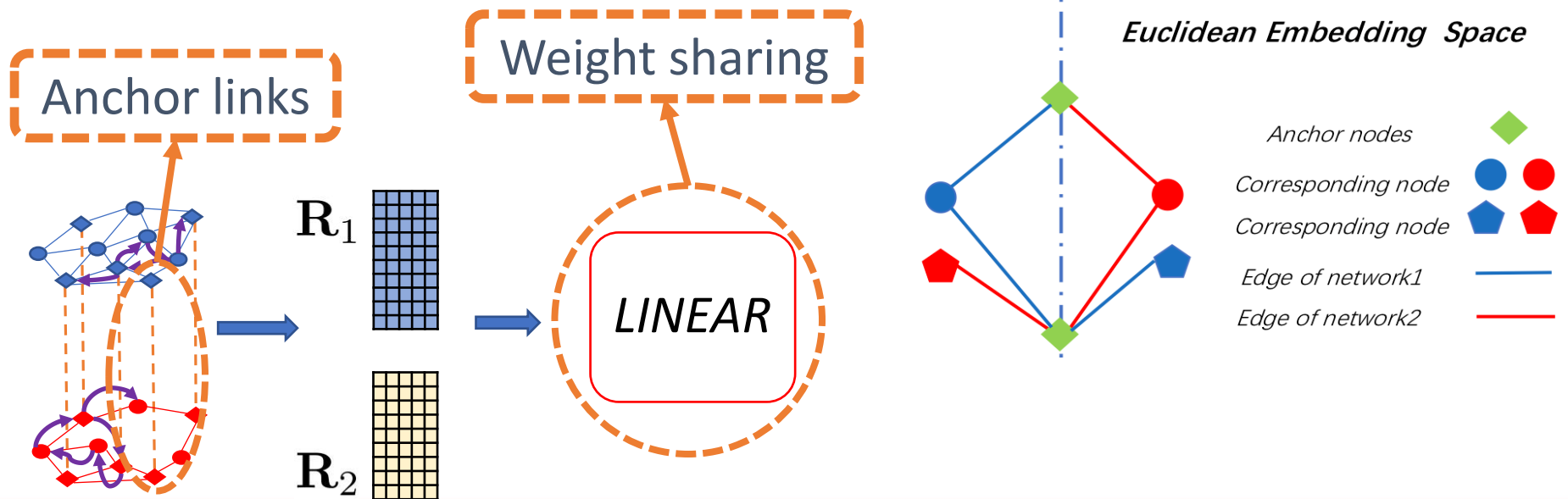
Key Idea #1: RWR for Flexible Propagation

- Drawbacks for consistency optimization based methods
 - Exactly same steps
 - Random walk with restart allows **restart**.
 - Equal weight for all anchor links
 - Linear layer trains **different weights**.



Key Idea #2: Build a Unified Space

- Drawbacks for embedding based methods
 - Space disparity
 - (1) Anchor links as basis
 - (2) Weight sharing



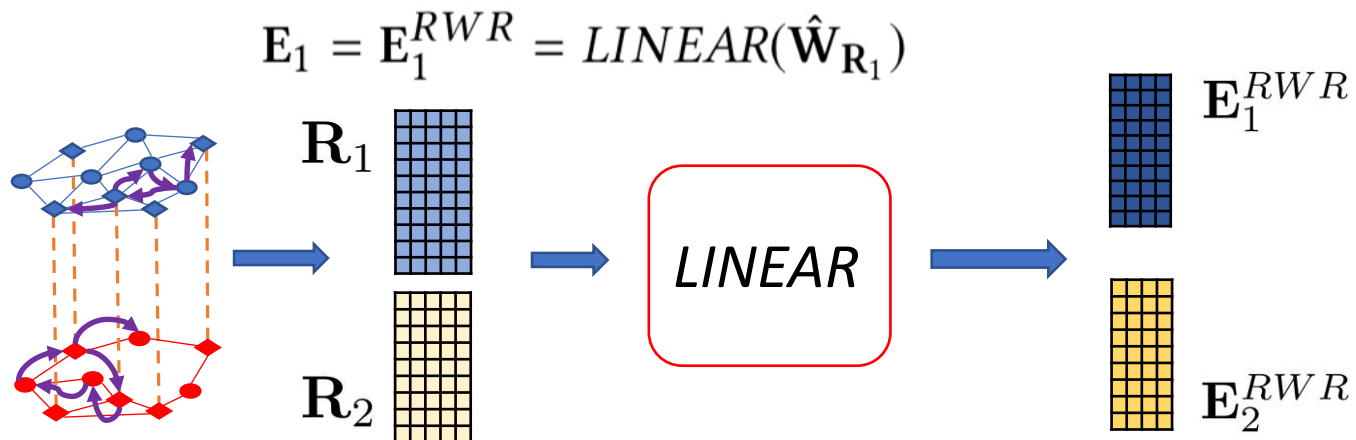
Part #1: BRIGHT-U (Plain Network)

- RWR from anchor links

$$\mathbf{r}_{l_1} = (1 - \beta)\hat{\mathbf{W}}_1\mathbf{r}_{l_1} + \beta\mathbf{e}_{l_1} \quad \hat{\mathbf{W}}_1 = (\mathbf{D}^{-1}\mathbf{A}_1)^T$$

$$\mathbf{r}_{l_1} = \beta(\mathbf{I} - (1 - \beta)\hat{\mathbf{W}}_1)^{-1}\mathbf{e}_{l_1}$$

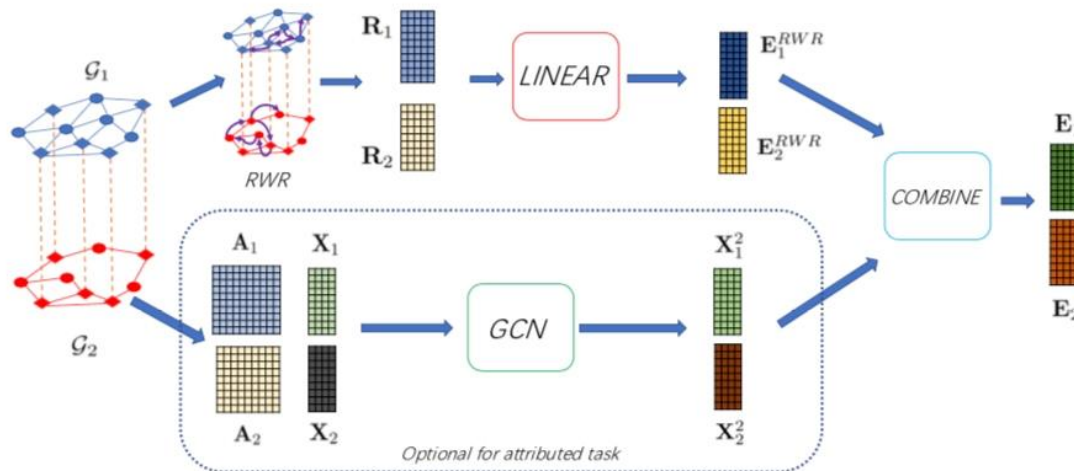
- Put all \mathbf{r}_{l_i} together as RWR embedding matrix $\hat{\mathbf{W}}_{R_1}$
- Use a shared linear layer to adjust anchor link weights



Part #2: BRIGHT-A (Attributed Network)

- Compute RWR embedding same as BRIGHT-U
- Use a shared two-layer GCN to capture attribute
- Combine RWR embedding and GCN embedding

$$E_1 = \text{COMBINE}([E_1^{RWR} || X_1^2])$$



Part #3: Model Training

- Ranking loss

$$\mathcal{J}_i = \frac{1}{|\mathcal{L}|} \sum_{l \in \mathcal{L}} \frac{1}{|U_{l_i}|} \sum_{u \in U_{l_i}} \max\{0, \gamma + d(l_1, l_2) - d(l_i, u)\}$$

$$\mathcal{J} = \mathcal{J}_1 + \mathcal{J}_2$$

- Advanced negative sampling
 - Sort-then-select
- Construct the alignment matrix

$$S(x, a) = e^{-d(x, a)}$$



Outline

- Introduction
- Theoretical Analysis
- Proposed Model ✓
- **Experimental Results**
- Conclusions

Experimental Setup

- Datasets

| Categories | Networks | # of Nodes | # of Edges | # of Attributes |
|---------------------|-------------------|------------|------------|-----------------|
| Plain Networks | <i>Foursquare</i> | 5,313 | 54,233 | — |
| | <i>Twitter</i> | 5,120 | 130,575 | — |
| | <i>ACM</i> | 9,916 | 44,808 | — |
| | <i>DBLP</i> | 9,872 | 39,561 | — |
| Attributed Networks | <i>ACM(A)</i> | 9,916 | 44,808 | 17 |
| | <i>DBLP(A)</i> | 9,872 | 39,561 | 17 |
| | <i>Cora-1</i> | 2,708 | 5,806 | 1,433 |
| | <i>Cora-2</i> | 2,708 | 4,547 | 1,433 |

- Metrics: Hit@K, MRR
- Baseline methods:
 - Plain network: CrossMNA, IONE, FINAL-P
 - Attributed network: REGAL, FINAL-N, NetTrans

Experimental Results-Alignment

| Plain Task | <i>DBLP vs. ACM</i> | | | | <i>Foursquare vs. Twitter</i> | | | |
|-----------------|---------------------------|---------------|---------------|---------------|-------------------------------|---------------|---------------|---------------|
| Metrics | Hit@1 | Hit@10 | Hit@30 | MRR | Hit@1 | Hit@10 | Hit@30 | MRR |
| CrossMNA | 7.90% | 62.53% | 79.48% | 23.42% | 0.00% | 3.26% | 12.03% | 1.48% |
| IONE | 30.91% | 74.25% | 84.11% | 46.26% | 4.50% | 16.69% | 27.80% | 8.56% |
| FINAL-P | 19.49% | 68.75% | 81.23% | 35.00% | 4.97% | 22.22% | 32.25% | 10.31% |
| BRIGHT-U | <u>40.45%</u> | <u>81.26%</u> | <u>84.13%</u> | <u>53.85%</u> | <u>6.37%</u> | <u>25.24%</u> | <u>33.54%</u> | <u>13.04%</u> |
| Attributed Task | <i>DBLP(A) vs. ACM(A)</i> | | | | <i>Cora-1 vs. Cora-2</i> | | | |
| Metrics | Hit@1 | Hit@10 | Hit@30 | MRR | Hit@1 | Hit@10 | Hit@30 | MRR |
| REGAL | 36.26% | 60.36% | 69.51% | 44.92% | 45.66% | 60.90% | 69.21% | 51.11% |
| FINAL-N | 38.18% | 79.74% | 89.07% | 52.15% | <u>86.29%</u> | 91.32% | 91.37% | 88.70% |
| NetTrans | 11.84% | 84.11% | <u>94.53%</u> | 30.11% | 27.56% | 90.95% | 97.51% | 49.67% |
| BRIGHT-A | <u>45.26%</u> | <u>86.76%</u> | 92.17% | <u>59.87%</u> | 83.85% | <u>99.08%</u> | <u>99.68%</u> | <u>90.41%</u> |

Observation: (1) An advantage of 10% in Hit@1 on *DBLP vs. ACM*;
 (2) 99% in Hit@10 on Cora.

Experimental Results-Ablation Study

| plain Task | <i>DBLP vs. ACM</i> | | <i>Foursquare vs. Twitter</i> | |
|---------------|---------------------|---------------|-------------------------------|---------------|
| Metrics | Hit@10 | MRR | Hit@10 | MRR |
| BRIGHT-U(SPD) | 75.75% | 48.78% | 6.06% | 3.07% |
| BRIGHT-U | <u>81.26%</u> | <u>53.85%</u> | <u>25.24%</u> | <u>13.04%</u> |

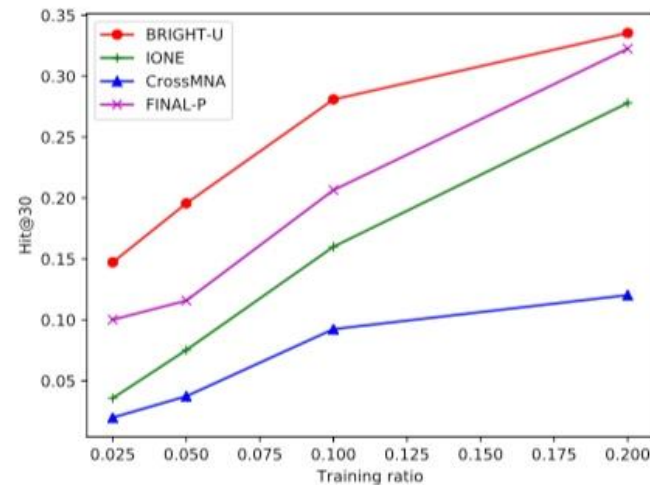
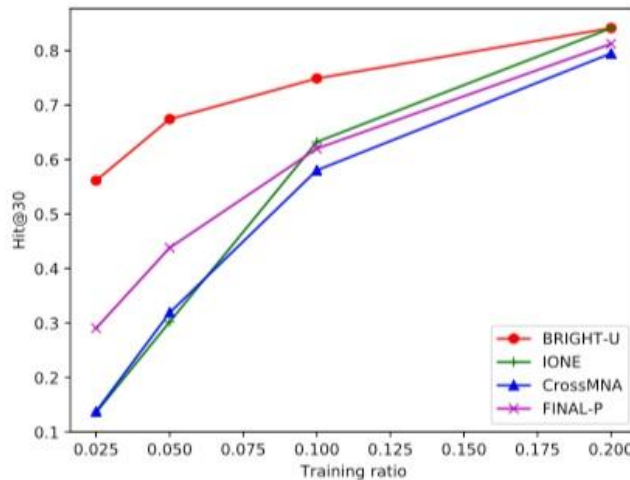
Ablation Study for BRIGHT-U

| Attributed Task | <i>DBLP(A) vs. ACM(A)</i> | | <i>Cora-1 vs. Cora-2</i> | |
|---------------------|---------------------------|---------------|--------------------------|---------------|
| Metrics | Hit@10 | MRR | Hit@10 | MRR |
| BRIGHT-A(-RWR) | 79.43% | 51.61% | <u>99.08%</u> | 90.12% |
| BRIGHT-A(-RWR:3500) | 84.31% | 58.01% | <u>99.08%</u> | 90.12% |
| BRIGHT-A | <u>86.76%</u> | <u>59.87%</u> | <u>99.08%</u> | <u>90.41%</u> |

Ablation Study for BRIGHT-A

Observation: (1) RWR module performs better than SPD;
 (2) Attribute plays an important role in BRIGHT-A.

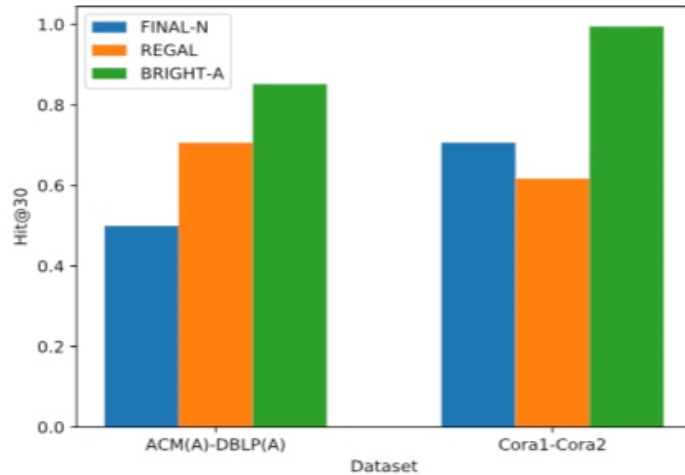
Experimental Results-Small Training Ratio



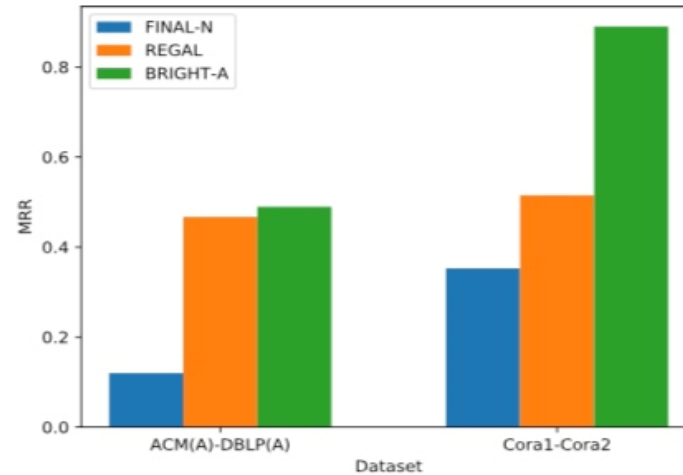
(a) Hit@30 with small training ratio on **S1** (b) Hit@30 with small training ratio on **S2**.

Observation: (1) Perform well under small training ratio;
 (2) Avoid the space disparity issue better.

Experimental Results-Unsupervised Setting



(a) Hit@30



(b) MRR

Observation: Good generalization to unsupervised setting.

Outline

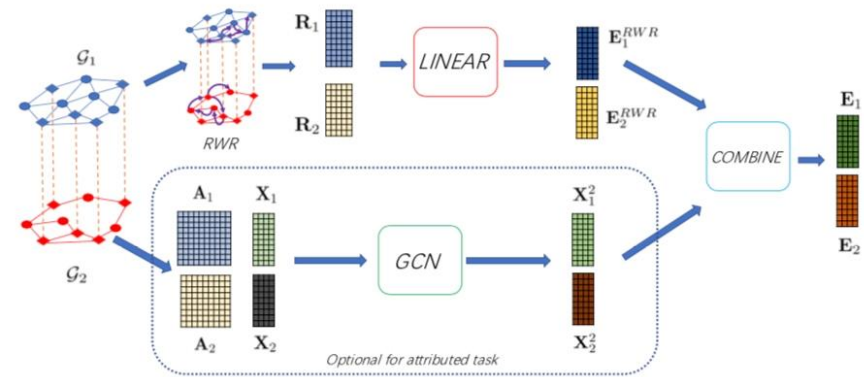
- Introduction
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- **Conclusions**

Conclusions

Problem: Network Alignment

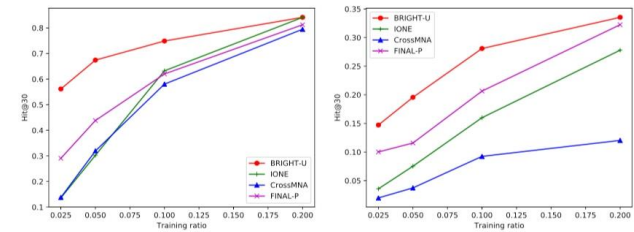
Solution:

- BRIGHT-U
 - RWR for flexible propagation
 - Anchor link as basis
 - Weight sharing
- BRIGHT-A
 - Shared GCN to capture attribute

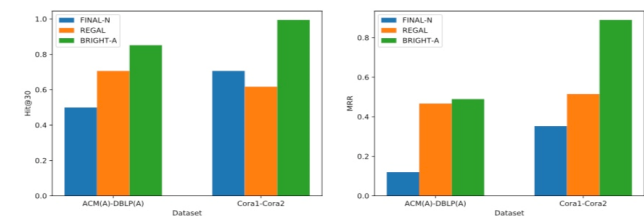


Results:

- Outperform all baselines
- Perform well with small training ratio
- Generalization to unsupervised setting



(a) Hit@30 with small training ratio on $S1$ (b) Hit@30 with small training ratio on $S2$.



(a) Hit@30 (b) MRR